SEQUENCE LISTING

<110> DOI, Hirofumi
WADA, Naoya
NAKAJIMA, Hiroto

<120> c-Jun phosphorylation inhibitor

<130> 3190-066

<140> US Unassigned
<141> 2004-09-27

<150> PCT/JP03/04120
<151> 2003-03-31

<150> JP P2002-095291
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Met Ala Pro Gly Thr Gly Ser Ser Thr Ala Val Asn Ser Cys Ser Pro
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Gln Ser Leu Ser Ser Val Leu Gly Ser Gly Phe Gly Glu Leu Ala Pro
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Pro Lys Met Ala Asn Ile Thr Ser Ser Gln Ile Leu Asp Gln Leu Lys
35 40 45

Ala Pro Ser Leu Gly Gln Phe Thr Thr Thr Pro Ser Thr Gln Gln Asn
50 55 60

Ser Thr Ser His Pro Thr Thr Thr Thr Ser Trp Asp Leu Lys Pro Pro
65 70 75 80

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Thr Ser Gln Ser Ser Val Leu Ser His Leu Asp Phe Lys Ser Gln Pro
                85                  90                  95

Glu Pro Ser Pro Val Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln
            100                 105                 110

Ser Gln Ala Val Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser
        115                 120                 125

Gln Ala Lys Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val
    130                 135                 140

Asn Lys Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val
145                 150                 155                 160

Ser Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
                165                 170                 175

Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro Gly
            180                 185                 190

Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu Glu Phe
        195                 200                 205

Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro Ser Ser Glu
    210                 215                 220

Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys Ser Leu Ser Glu
225                 230                 235                 240

Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala Val Gln Asn Ser Thr
                245                 250                 255

Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser Leu Thr Ser Ser Ser Leu
            260                 265                 270

Asn Ser Ala Ser Pro Val Ala Met Ser Ser Ser Tyr Asp Gln Ser Ser
        275                 280                 285

Val His Asn Arg Ile Pro Tyr Gln Ser Pro Val Ser Ser Ser Glu Ser
    290                 295                 300
```

Ala Pro Gly Thr Ile Met Asn Gly His Gly Gly Gly Arg Ser Gln Gln
305 310 315 320

Thr Leu Asp Thr Pro Lys Thr Thr Gly Pro Pro Ser Ala Leu Pro Ser
325 330 335

Val Ser Ser Leu Pro Ser Thr Thr Ser Cys Thr Ala Leu Leu Pro Ser
340 345 350

Thr Ser Gln His Thr Gly Asp Leu Thr Ser Ser Pro Leu Ser Gln Leu
355 360 365

Ser Ser Ser Leu Ser Ser His Gln Ser Ser Leu Ser Ala His Ala Ala
370 375 380

Leu Ser Ser Ser Thr Ser His Thr His Ala Ser Val Glu Ser Ala Ser
385 390 395 400

Ser His Gln Ser Ser Ala Thr Phe Ser Thr Ala Ala Thr Ser Val Ser
405 410 415

Ser Ser Ala Ser Ser Gly Val Ser Leu Ser Ser Ser Met Asn Thr Ala
420 425 430

Asn Ser Leu Cys Leu Gly Gly Thr Pro Ala Ser Ala Ser Ser Ser Ser
435 440 445

Ser Arg Ala Ala Pro Leu Val Thr Ser Gly Lys Ala Pro Pro Asn Leu
450 455 460

Pro Gln Gly Val Pro Pro Leu Leu His Asn Gln Tyr Leu Val Gly Pro
465 470 475 480

Gly Gly Leu Leu Pro Ala Tyr Pro Ile Tyr Gly Tyr Asp Glu Leu Gln
485 490 495

Met Leu Gln Ser Arg Leu Pro Val Asp Tyr Tyr Gly Ile Pro Phe Ala
500 505 510

Ala Pro Thr Ala Leu Ala Ser Arg Asp Arg Ser Leu Ala Asn Asn Pro
515 520 525

Tyr Pro Gly Asp Val Thr Lys Phe Gly Arg Gly Asp Ser Ala Ser Pro
530 535 540

Ala Pro Ala Thr Thr Pro Ala Gln Pro Gln Gln Ser Gln Ser Gln Thr
545 550 555 560

His His Thr Ala Gln Gln Pro Phe Val Asn Pro Ala Leu Pro Pro Gly
565 570 575

Tyr Ser Tyr Thr Gly Leu Pro Tyr Tyr Thr Gly Met Pro Ser Ala Phe
580 585 590

Gln Tyr Gly Pro Thr Met Phe Val Pro Pro Ala Ser Ala Lys Gln His
595 600 605

Gly Val Asn Leu Ser Thr Pro Thr Pro Pro Phe Gln Gln Ala Ser Gly
610 615 620

Tyr Gly Gln His Gly Tyr Ser Thr Gly Tyr Asp Asp Leu Thr Gln Gly
625 630 635 640

Thr Ala Ala Gly Asp Tyr Ser Lys Gly Gly Tyr Ala Gly Ser Ser Gln
645 650 655

Ala Pro Asn Lys Ser Ala Gly Ser Gly Pro Gly Lys Gly Val Ser Val
660 665 670

Ser Ser Ser Thr Thr Gly Leu Pro Asp Met Thr Gly Ser Val Tyr Asn
675 680 685

Lys Thr Gln Thr Phe Asp Lys Gln Gly Phe His Ala Gly Thr Pro Pro
690 695 700

Pro Phe Ser Leu Pro Ser Val Leu Gly Ser Thr Gly Pro Leu Ala Ser
705 710 715 720

Gly Ala Ala Pro Gly Tyr Ala Pro Pro Pro Phe Leu His Ile Leu Pro
725 730 735

Ala His Gln Gln Pro His Ser Gln Leu Leu His His His Leu Pro Gln
740 745 750

Asp Ala Gln Ser Gly Ser Gly Gln Arg Ser Gln Pro Ser Ser Leu Gln
755 760 765

Pro Lys Ser Gln Ala Ser Lys Pro Ala Tyr Gly Asn Ser Pro Tyr Trp
770 775 780

Thr Asn
785

<210> 2
<211> 579
<212> PRT
<213> Homo sapiens

<400> 2

Leu Ser Gln Glu Glu Gly Val Phe Ala Gln Asp Leu Glu Pro Ala Pro
1 5 10 15

Ile Glu Asp Gly Ile Val Tyr Pro Glu Pro Ser Asp Asn Pro Thr Met
20 25 30

Asp Thr Ser Glu Phe Gln Val Gln Ala Pro Ala Arg Gly Thr Leu Gly
35 40 45

Arg Val Tyr Pro Gly Ser Arg Ser Ser Glu Lys His Ser Pro Asp Ser
50 55 60

Ala Cys Ser Val Asp Tyr Ser Ser Ser Cys Leu Ser Ser Pro Glu His
65 70 75 80

Pro Thr Glu Asp Ser Glu Ser Thr Glu Pro Leu Ser Val Asp Gly Ile
85 90 95

Ser Ser Asp Leu Glu Glu Pro Ala Glu Gly Asp Glu Glu Glu Glu Glu
100 105 110

Glu Glu Gly Gly Met Gly Pro Tyr Gly Leu Gln Glu Gly Ser Pro Gln
115 120 125

Thr Pro Asp Gln Glu Gln Phe Leu Lys Gln His Phe Glu Thr Leu Ala
130 135 140

Ser Gly Ala Ala Pro Gly Ala Pro Val Gln Val Pro Glu Arg Ser Glu

145 150 155 160

Ser Arg Ser Ile Ser Ser Arg Phe Leu Leu Gln Val Gln Thr Arg Pro
165 170 175

Leu Arg Glu Pro Ser Pro Ser Ser Ser Ser Leu Ala Leu Met Ser Arg
180 185 190

Pro Ala Gln Val Pro Gln Ala Ser Gly Glu Gln Pro Arg Gly Asn Gly
195 200 205

Ala Asn Pro Pro Gly Ala Pro Pro Glu Val Glu Pro Ser Ser Gly Asn
210 215 220

Pro Ser Pro Gln Gln Ala Ala Ser Val Leu Leu Pro Arg Cys Arg Leu
225 230 235 240

Asn Pro Asp Ser Ser Trp Ala Pro Lys Arg Val Ala Thr Ala Ser Pro
245 250 255

Phe Ser Gly Leu Gln Lys Ala Gln Ser Val His Ser Leu Val Pro Gln
260 265 270

Glu Arg His Glu Ala Ser Leu Gln Ala Pro Ser Pro Gly Ala Leu Leu
275 280 285

Ser Arg Glu Ile Glu Ala Gln Asp Gly Leu Gly Ser Leu Pro Pro Ala
290 295 300

Asp Gly Pro Pro Ser Arg Pro His Ser Tyr Gln Asn Pro Thr Thr Ser
305 310 315 320

Ser Met Ala Lys Ile Ser Arg Ser Ile Ser Val Gly Glu Asn Leu Gly
325 330 335

Leu Val Ala Glu Pro Gln Ala His Ala Pro Ile Arg Val Ser Pro Leu
340 345 350

Ser Lys Leu Ala Leu Pro Ser Arg Ala His Leu Val Leu Asp Ile Pro
355 360 365

Lys Pro Leu Pro Asp Arg Pro Thr Leu Ala Ala Phe Ser Pro Val Thr

370 375 380

Lys Gly Arg Ala Pro Gly Glu Ala Glu Lys Pro Gly Phe Pro Val Gly
385 390 395 400

Leu Gly Lys Ala His Ser Thr Thr Glu Arg Trp Ala Cys Leu Gly Glu
405 410 415

Gly Thr Thr Pro Lys Pro Arg Thr Glu Cys Gln Ala His Pro Gly Pro
420 425 430

Ser Ser Pro Cys Ala Gln Gln Leu Pro Val Ser Ser Leu Phe Gln Gly
435 440 445

Pro Glu Asn Leu Gln Pro Pro Pro Pro Glu Lys Thr Pro Asn Pro Met
450 455 460

Glu Cys Thr Lys Pro Gly Ala Ala Leu Ser Gln Asp Ser Ala Val Ser
465 470 475 480

Leu Glu Gln Cys Glu Gln Leu Val Ala Glu Leu Arg Gly Ser Val Arg
485 490 495

Gln Ala Val Arg Leu Tyr His Ser Val Ala Gly Cys Lys Met Pro Ser
500 505 510

Ala Glu Gln Ser Arg Ile Ala Gln Leu Leu Arg Asp Thr Phe Ser Ser
515 520 525

Val Arg Gln Glu Leu Glu Ala Val Ala Gly Ala Val Leu Ser Ser Pro
530 535 540

Gly Ser Ser Pro Gly Ala Val Gly Ala Glu Gln Thr Gln Ala Leu Leu
545 550 555 560

Glu Gln Tyr Ser Glu Leu Leu Leu Arg Ala Val Glu Arg Arg Met Glu
565 570 575

Arg Lys Leu

<210> 3
<211> 1217

<212> PRT
<213> Homo sapiens

<400> 3

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Ser Asn Lys Val Ser Ser Arg Val Thr Ala Val Ser Phe Ser Glu Asp
1               5                  10                  15

Cys Ser Tyr Phe Val Thr Ala Gly Asn Arg His Ile Lys Phe Trp Tyr
            20                  25                  30

Leu Asp Asp Ser Lys Thr Ser Lys Val Asn Ala Thr Val Pro Leu Leu
        35                  40                  45

Gly Arg Ser Gly Leu Leu Gly Glu Leu Arg Asn Asn Leu Phe Thr Asp
    50                  55                  60

Val Ala Cys Gly Arg Gly Lys Lys Ala Asp Ser Thr Phe Cys Ile Thr
65                  70                  75                  80

Ser Ser Gly Leu Leu Cys Glu Phe Ser Asp Arg Arg Leu Leu Asp Lys
                85                  90                  95

Trp Val Glu Leu Arg Val Tyr Pro Glu Val Lys Asp Ser Asn Gln Ala
            100                 105                 110

Cys Leu Pro Pro Ser Ser Phe Ile Thr Cys Ser Ser Asp Asn Thr Ile
        115                 120                 125

Arg Leu Trp Asn Thr Glu Ser Ser Gly Val His Gly Ser Thr Leu His
    130                 135                 140

Arg Asn Ile Leu Ser Ser Asp Leu Ile Lys Ile Ile Tyr Val Asp Gly
145                 150                 155                 160

Asn Thr Gln Ala Leu Leu Asp Thr Glu Leu Pro Gly Gly Asp Lys Ala
                165                 170                 175

Asp Ala Ser Leu Leu Asp Pro Arg Val Gly Ile Arg Ser Val Cys Val
            180                 185                 190

Ser Pro Asn Gly Gln His Leu Ala Ser Gly Asp Arg Met Gly Thr Leu
        195                 200                 205
```

Arg Val His Glu Leu Gln Ser Leu Ser Glu Met Leu Lys Val Glu Ala
210 215 220

His Asp Ser Glu Ile Leu Cys Leu Glu Tyr Ser Lys Pro Asp Thr Gly
225 230 235 240

Leu Lys Leu Leu Ala Ser Ala Ser Arg Asp Arg Leu Ile His Val Leu
245 250 255

Asp Ala Gly Arg Glu Tyr Ser Leu Gln Gln Thr Leu Asp Glu His Ser
260 265 270

Ser Ser Ile Thr Ala Val Lys Phe Ala Ala Ser Asp Gly Gln Val Arg
275 280 285

Met Ile Ser Cys Gly Ala Asp Lys Ser Ile Tyr Phe Arg Thr Ala Gln
290 295 300

Lys Ser Gly Asp Gly Val Gln Phe Thr Arg Thr His His Val Val Arg
305 310 315 320

Lys Thr Thr Leu Tyr Asp Met Asp Val Glu Pro Ser Trp Lys Tyr Thr
325 330 335

Ala Ile Gly Cys Gln Asp Arg Asn Ile Arg Ile Phe Asn Ile Ser Ser
340 345 350

Gly Lys Gln Lys Lys Leu Phe Lys Gly Ser Gln Gly Glu Asp Gly Thr
355 360 365

Leu Ile Lys Val Gln Thr Asp Pro Ser Gly Ile Tyr Ile Ala Thr Ser
370 375 380

Cys Ser Asp Lys Asn Leu Ser Ile Phe Asp Phe Ser Ser Gly Glu Cys
385 390 395 400

Val Ala Thr Met Phe Gly His Ser Glu Ile Val Thr Gly Met Lys Phe
405 410 415

Ser Asn Asp Cys Lys His Leu Ile Ser Val Ser Gly Asp Ser Cys Ile
420 425 430

Phe Val Trp Arg Leu Ser Ser Glu Met Thr Ile Ser Met Arg Gln Arg
435 440 445

Leu Ala Glu Leu Arg Gln Arg Gln Arg Gly Gly Lys Gln Gln Gly Pro
450 455 460

Ser Ser Pro Gln Arg Ala Ser Gly Pro Asn Arg His Gln Ala Pro Ser
465 470 475 480

Met Leu Ser Pro Gly Pro Ala Leu Ser Ser Asp Ser Asp Lys Glu Gly
485 490 495

Glu Asp Glu Gly Thr Glu Glu Glu Leu Pro Ala Leu Pro Val Leu Ala
500 505 510

Lys Ser Thr Lys Lys Ala Leu Ala Ser Val Pro Ser Pro Ala Leu Pro
515 520 525

Arg Ser Leu Ser His Trp Glu Met Ser Arg Ala Gln Glu Ser Val Gly
530 535 540

Phe Leu Asp Pro Ala Pro Ala Ala Asn Pro Gly Pro Arg Arg Arg Gly
545 550 555 560

Arg Trp Val Gln Pro Gly Val Glu Leu Ser Val Arg Ser Met Leu Asp
565 570 575

Leu Arg Gln Leu Glu Thr Leu Ala Pro Ser Leu Gln Asp Pro Ser Gln
580 585 590

Asp Ser Leu Ala Ile Ile Pro Ser Gly Pro Arg Lys His Gly Gln Glu
595 600 605

Ala Leu Glu Thr Ser Leu Thr Ser Gln Asn Glu Lys Pro Pro Arg Pro
610 615 620

Gln Ala Ser Gln Pro Cys Ser Tyr Pro His Ile Ile Arg Leu Leu Ser
625 630 635 640

Gln Glu Glu Gly Val Phe Ala Gln Asp Leu Glu Pro Ala Pro Ile Glu
645 650 655

Asp Gly Ile Val Tyr Pro Glu Pro Ser Asp Asn Pro Thr Met Asp Thr

660 665 670

Ser Glu Phe Gln Val Gln Ala Pro Ala Arg Gly Thr Leu Gly Arg Val
675 680 685

Tyr Pro Gly Ser Arg Ser Ser Glu Lys His Ser Pro Asp Ser Ala Cys
690 695 700

Ser Val Asp Tyr Ser Ser Ser Cys Leu Ser Ser Pro Glu His Pro Thr
705 710 715 720

Glu Asp Ser Glu Ser Thr Glu Pro Leu Ser Val Asp Gly Ile Ser Ser
725 730 735

Asp Leu Glu Glu Pro Ala Glu Gly Asp Glu Glu Glu Glu Glu Glu Glu
740 745 750

Gly Gly Met Gly Pro Tyr Gly Leu Gln Glu Gly Ser Pro Gln Thr Pro
755 760 765

Asp Gln Glu Gln Phe Leu Lys Gln His Phe Glu Thr Leu Ala Ser Gly
770 775 780

Ala Ala Pro Gly Ala Pro Val Gln Val Pro Glu Arg Ser Glu Ser Arg
785 790 795 800

Ser Ile Ser Ser Arg Phe Leu Leu Gln Val Gln Thr Arg Pro Leu Arg
805 810 815

Glu Pro Ser Pro Ser Ser Ser Ser Leu Ala Leu Met Ser Arg Pro Ala
820 825 830

Gln Val Pro Gln Ala Ser Gly Glu Gln Pro Arg Gly Asn Gly Ala Asn
835 840 845

Pro Pro Gly Ala Pro Pro Glu Val Glu Pro Ser Ser Gly Asn Pro Ser
850 855 860

Pro Gln Gln Ala Ala Ser Val Leu Leu Pro Arg Cys Arg Leu Asn Pro
865 870 875 880

Asp Ser Ser Trp Ala Pro Lys Arg Val Ala Thr Ala Ser Pro Phe Ser

885 890 895

Gly Leu Gln Lys Ala Gln Ser Val His Ser Leu Val Pro Gln Glu Arg
900 905 910

His Glu Ala Ser Leu Gln Ala Pro Ser Pro Gly Ala Leu Leu Ser Arg
915 920 925

Glu Ile Glu Ala Gln Asp Gly Leu Gly Ser Leu Pro Pro Ala Asp Gly
930 935 940

Pro Pro Ser Arg Pro His Ser Tyr Gln Asn Pro Thr Thr Ser Ser Met
945 950 955 960

Ala Lys Ile Ser Arg Ser Ile Ser Val Gly Glu Asn Leu Gly Leu Val
965 970 975

Ala Glu Pro Gln Ala His Ala Pro Ile Arg Val Ser Pro Leu Ser Lys
980 985 990

Leu Ala Leu Pro Ser Arg Ala His Leu Val Leu Asp Ile Pro Lys Pro
995 1000 1005

Leu Pro Asp Arg Pro Thr Leu Ala Ala Phe Ser Pro Val Thr Lys
1010 1015 1020

Gly Arg Ala Pro Gly Glu Ala Glu Lys Pro Gly Phe Pro Val Gly
1025 1030 1035

Leu Gly Lys Ala His Ser Thr Thr Glu Arg Trp Ala Cys Leu Gly
1040 1045 1050

Glu Gly Thr Thr Pro Lys Pro Arg Thr Glu Cys Gln Ala His Pro
1055 1060 1065

Gly Pro Ser Ser Pro Cys Ala Gln Gln Leu Pro Val Ser Ser Leu
1070 1075 1080

Phe Gln Gly Pro Glu Asn Leu Gln Pro Pro Pro Pro Glu Lys Thr
1085 1090 1095

Pro Asn Pro Met Glu Cys Thr Lys Pro Gly Ala Ala Leu Ser Gln

1100 1105 1110

Asp Ser Ala Val Ser Leu Glu Gln Cys Glu Gln Leu Val Ala Glu
1115 1120 1125

Leu Arg Gly Ser Val Arg Gln Ala Val Arg Leu Tyr His Ser Val
1130 1135 1140

Ala Gly Cys Lys Met Pro Ser Ala Glu Gln Ser Arg Ile Ala Gln
1145 1150 1155

Leu Leu Arg Asp Thr Phe Ser Ser Val Arg Gln Glu Leu Glu Ala
1160 1165 1170

Val Ala Gly Ala Val Leu Ser Ser Pro Gly Ser Ser Pro Gly Ala
1175 1180 1185

Val Gly Ala Glu Gln Thr Gln Ala Leu Leu Glu Gln Tyr Ser Glu
1190 1195 1200

Leu Leu Leu Arg Ala Val Glu Arg Arg Met Glu Arg Lys Leu
1205 1210 1215

<210> 4
<211> 626
<212> PRT
<213> Homo sapiens

<400> 4

Met Ala Asp Gln Arg Met Asp Ile Ser Ser Thr Ile Ser Asp Phe Met
1 5 10 15

Ser Pro Gly Pro Thr Asp Leu Leu Ser Ser Ser Leu Gly Thr Ser Gly
20 25 30

Val Asp Cys Asn Arg Lys Arg Lys Gly Ser Ser Thr Asp Tyr Gln Glu
35 40 45

Ser Met Asp Thr Asp Lys Asp Asp Pro His Gly Arg Leu Glu Tyr Thr
50 55 60

Glu His Gln Gly Arg Ile Lys Asn Ala Arg Glu Ala His Ser Gln Ile
65 70 75 80

```
Glu Lys Arg Arg Arg Asp Lys Met Asn Ser Phe Ile Asp Glu Leu Ala
                85                  90                  95

Ser Leu Val Pro Thr Cys Asn Ala Met Ser Arg Lys Leu Asp Lys Leu
            100                 105                 110

Thr Val Leu Arg Met Ala Val Gln His Met Lys Thr Leu Arg Gly Ala
        115                 120                 125

Thr Asn Pro Tyr Thr Glu Ala Asn Tyr Lys Pro Thr Phe Leu Ser Asp
    130                 135                 140

Asp Glu Leu Lys His Leu Ile Leu Arg Ala Ala Asp Gly Phe Leu Phe
145                 150                 155                 160

Val Val Gly Cys Asp Arg Gly Lys Ile Leu Phe Val Ser Glu Ser Val
                165                 170                 175

Phe Lys Ile Leu Asn Tyr Ser Gln Asn Asp Leu Ile Gly Gln Ser Leu
            180                 185                 190

Phe Asp Tyr Leu His Pro Lys Asp Ile Ala Lys Val Lys Glu Gln Leu
        195                 200                 205

Ser Ser Ser Asp Thr Ala Pro Arg Glu Arg Leu Ile Asp Ala Lys Thr
    210                 215                 220

Gly Leu Pro Val Lys Thr Asp Ile Thr Pro Gly Pro Ser Arg Leu Cys
225                 230                 235                 240

Ser Gly Ala Arg Arg Ser Phe Phe Cys Arg Met Lys Cys Asn Arg Pro
                245                 250                 255

Ser Val Lys Val Glu Asp Lys Asp Phe Pro Ser Thr Cys Ser Lys Lys
            260                 265                 270

Lys Ala Asp Arg Lys Ser Phe Cys Thr Ile His Ser Thr Gly Tyr Leu
        275                 280                 285

Lys Ser Trp Pro Pro Thr Lys Met Gly Leu Asp Glu Asp Asn Glu Pro
    290                 295                 300
```

```
Asp Asn Glu Gly Cys Asn Leu Ser Cys Leu Val Ala Ile Gly Arg Leu
305                 310                 315                 320

His Ser His Val Val Pro Gln Pro Val Asn Gly Glu Ile Arg Val Lys
                325                 330                 335

Ser Met Glu Tyr Val Ser Arg His Ala Ile Asp Gly Lys Phe Val Phe
            340                 345                 350

Val Asp Gln Arg Ala Thr Ala Ile Leu Ala Tyr Leu Pro Gln Glu Leu
        355                 360                 365

Leu Gly Thr Ser Cys Tyr Glu Tyr Phe His Gln Asp Asp Ile Gly His
    370                 375                 380

Leu Ala Glu Cys His Arg Gln Val Leu Gln Thr Arg Glu Lys Ile Thr
385                 390                 395                 400

Thr Asn Cys Tyr Lys Phe Lys Ile Lys Asp Gly Ser Phe Ile Thr Leu
                405                 410                 415

Arg Ser Arg Trp Phe Ser Phe Met Asn Pro Trp Thr Lys Glu Val Glu
            420                 425                 430

Tyr Ile Val Ser Thr Asn Thr Val Val Leu Ala Asn Val Leu Glu Gly
        435                 440                 445

Gly Asp Pro Thr Phe Pro Gln Leu Thr Ala Ser Pro His Ser Met Asp
    450                 455                 460

Ser Met Leu Pro Ser Gly Glu Gly Gly Pro Lys Arg Thr His Pro Thr
465                 470                 475                 480

Val Pro Gly Ile Pro Gly Gly Thr Arg Ala Gly Ala Gly Lys Ile Gly
                485                 490                 495

Arg Met Ile Ala Glu Glu Ile Met Glu Ile His Arg Ile Arg Gly Ser
            500                 505                 510

Ser Pro Ser Ser Cys Gly Ser Ser Pro Leu Asn Ile Thr Ser Thr Pro
        515                 520                 525
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```
Pro Pro Asp Ala Ser Ser Pro Gly Gly Lys Lys Ile Leu Asn Gly Gly
    530                 535                 540

Thr Pro Asp Ile Pro Ser Ser Gly Leu Leu Ser Gly Gln Ala Gln Glu
545                 550                 555                 560

Asn Pro Gly Tyr Pro Tyr Ser Asp Ser Ser Ser Ile Leu Gly Glu Asn
                565                 570                 575

Pro His Ile Gly Ile Asp Met Ile Asp Asn Asp Gln Gly Ser Ser Ser
            580                 585                 590

Pro Ser Asn Asp Glu Ala Ala Met Ala Val Ile Met Ser Leu Leu Glu
        595                 600                 605

Ala Asp Ala Gly Leu Gly Gly Pro Val Asp Phe Ser Asp Leu Pro Trp
    610                 615                 620

Pro Leu
625
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<210> 5
<211> 726
<212> PRT
<213> Homo sapiens

<400> 5

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Met Glu Asp Arg Leu His Met Asp Asn Gly Leu Val Pro Gln Lys Ile
1               5                   10                  15

Val Ser Val His Leu Gln Asp Ser Thr Leu Lys Glu Val Lys Asp Gln
            20                  25                  30

Val Ser Asn Lys Gln Ala Gln Ile Leu Glu Pro Lys Pro Glu Pro Ser
        35                  40                  45

Leu Glu Ile Lys Pro Glu Gln Asp Gly Met Glu His Val Gly Arg Asp
    50                  55                  60

Asp Pro Lys Ala Leu Gly Glu Glu Pro Lys Gln Arg Arg Gly Ser Ala
65                  70                  75                  80
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```
Ser Gly Ser Glu Pro Ala Gly Asp Ser Asp Arg Gly Gly Gly Pro Val
                85                  90                  95

Glu His Tyr His Leu His Leu Ser Ser Cys His Glu Cys Leu Glu Leu
            100                 105                 110

Glu Asn Ser Thr Ile Glu Ser Val Lys Phe Ala Ser Ala Glu Asn Ile
        115                 120                 125

Pro Asp Leu Pro Tyr Asp Tyr Ser Ser Ser Leu Glu Ser Val Ala Asp
    130                 135                 140

Glu Thr Ser Pro Glu Arg Glu Gly Arg Arg Val Asn Leu Thr Gly Lys
145                 150                 155                 160

Ala Pro Asn Ile Leu Leu Tyr Val Gly Ser Asp Ser Gln Glu Ala Leu
                165                 170                 175

Gly Arg Phe His Glu Val Arg Ser Val Leu Ala Asp Cys Val Asp Ile
            180                 185                 190

Asp Ser Tyr Ile Leu Tyr His Leu Leu Glu Asp Ser Ala Leu Arg Asp
        195                 200                 205

Pro Trp Thr Asp Asn Cys Leu Leu Leu Val Ile Ala Thr Arg Glu Ser
    210                 215                 220

Ile Pro Glu Asp Leu Tyr Gln Lys Phe Met Ala Tyr Leu Ser Gln Gly
225                 230                 235                 240

Gly Lys Val Leu Gly Leu Ser Ser Ser Phe Thr Phe Gly Gly Phe Gln
                245                 250                 255

Val Thr Ser Lys Gly Ala Leu His Lys Thr Val Gln Asn Leu Val Phe
            260                 265                 270

Ser Lys Ala Asp Gln Ser Glu Val Lys Leu Ser Val Leu Ser Ser Gly
        275                 280                 285

Cys Arg Tyr Gln Glu Gly Pro Val Arg Leu Ser Pro Gly Arg Leu Gln
    290                 295                 300

Gly His Leu Glu Asn Glu Asp Lys Asp Arg Met Ile Val His Val Pro
```

305 310 315 320

Phe Gly Thr Arg Gly Gly Glu Ala Val Leu Cys Gln Val His Leu Glu
325 330 335

Leu Pro Pro Ser Ser Asn Ile Val Gln Thr Pro Glu Asp Phe Asn Leu
340 345 350

Leu Lys Ser Ser Asn Phe Arg Arg Tyr Glu Val Leu Arg Glu Ile Leu
355 360 365

Thr Thr Leu Gly Leu Ser Cys Asp Met Lys Gln Val Pro Ala Leu Thr
370 375 380

Pro Leu Tyr Leu Leu Ser Ala Ala Glu Glu Ile Arg Asp Pro Leu Met
385 390 395 400

Gln Trp Leu Gly Lys His Val Asp Ser Glu Gly Glu Ile Lys Ser Gly
405 410 415

Gln Leu Ser Leu Arg Phe Val Ser Ser Tyr Val Ser Glu Val Glu Ile
420 425 430

Thr Pro Ser Cys Ile Pro Val Val Thr Asn Met Glu Ala Phe Ser Ser
435 440 445

Glu His Phe Asn Leu Glu Ile Tyr Arg Gln Asn Leu Gln Thr Lys Gln
450 455 460

Leu Gly Lys Val Ile Leu Phe Ala Glu Val Thr Pro Thr Thr Met Arg
465 470 475 480

Leu Leu Asp Gly Leu Met Phe Gln Thr Pro Gln Glu Met Gly Leu Ile
485 490 495

Val Ile Ala Ala Arg Gln Thr Glu Gly Lys Gly Arg Gly Gly Asn Val
500 505 510

Trp Leu Ser Pro Val Gly Cys Ala Leu Ser Thr Leu Leu Ile Ser Ile
515 520 525

Pro Leu Arg Ser Gln Leu Gly Gln Arg Ile Pro Phe Val Gln His Leu

530 535 540

Met Ser Val Ala Val Val Glu Ala Val Arg Ser Ile Pro Glu Tyr Gln
545 550 555 560

Asp Ile Asn Leu Arg Val Lys Trp Pro Asn Asp Ile Tyr Tyr Ser Asp
565 570 575

Leu Met Lys Ile Gly Gly Val Leu Val Asn Ser Thr Leu Met Gly Glu
580 585 590

Thr Phe Tyr Ile Leu Ile Gly Cys Gly Phe Asn Val Thr Asn Ser Asn
595 600 605

Pro Thr Ile Cys Ile Asn Asp Leu Ile Thr Glu Tyr Asn Lys Gln His
610 615 620

Lys Ala Glu Leu Lys Pro Leu Arg Ala Asp Tyr Leu Ile Ala Arg Val
625 630 635 640

Val Thr Val Leu Glu Lys Leu Ile Lys Glu Phe Gln Asp Lys Gly Pro
645 650 655

Asn Ser Val Leu Pro Leu Tyr Tyr Arg Tyr Trp Val His Ser Gly Gln
660 665 670

Gln Val His Leu Gly Ser Ala Glu Gly Pro Lys Val Ser Ile Val Gly
675 680 685

Leu Asp Asp Ser Gly Phe Leu Gln Val His Gln Glu Gly Gly Glu Val
690 695 700

Val Thr Val His Pro Asp Gly Asn Ser Phe Asp Met Leu Arg Asn Leu
705 710 715 720

Ile Leu Pro Lys Arg Arg
725

<210> 6
<211> 757
<212> PRT
<213> Homo sapiens

<400> 6

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Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser Gln Ile Leu Asp
1               5                  10                  15

Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr Thr Thr Pro Ser Thr
            20                  25                  30

Gln Gln Asn Ser Thr Ser His Pro Thr Thr Thr Thr Ser Trp Asp Leu
        35                  40                  45

Lys Pro Pro Thr Ser Gln Ser Ser Val Leu Ser His Leu Asp Phe Lys
    50                  55                  60

Ser Gln Pro Glu Pro Ser Pro Val Leu Ser Gln Leu Ser Gln Arg Gln
65                  70                  75                  80

Gln His Gln Ser Gln Ala Val Thr Val Pro Pro Pro Gly Leu Glu Ser
                85                  90                  95

Phe Pro Ser Gln Ala Lys Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro
            100                 105                 110

Ser Thr Val Asn Lys Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn
        115                 120                 125

Ile Ser Val Ser Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala
    130                 135                 140

Lys Arg Arg Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu
145                 150                 155                 160

Met Pro Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala
                165                 170                 175

Leu Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
            180                 185                 190

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys Ser
        195                 200                 205

Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala Val Gln
    210                 215                 220
```

```
Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser Leu Thr Ser
225                 230                 235                 240

Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser Ser Ser Tyr Asp
                245                 250                 255

Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln Ser Pro Val Ser Ser
            260                 265                 270

Ser Glu Ser Ala Pro Gly Thr Ile Met Asn Gly His Gly Gly Gly Arg
        275                 280                 285

Ser Gln Gln Thr Leu Asp Thr Pro Lys Thr Thr Gly Pro Pro Ser Ala
    290                 295                 300

Leu Pro Ser Val Ser Ser Leu Pro Ser Thr Thr Ser Cys Thr Ala Leu
305                 310                 315                 320

Leu Pro Ser Thr Ser Gln His Thr Gly Asp Leu Thr Ser Ser Pro Leu
                325                 330                 335

Ser Gln Leu Ser Ser Ser Leu Ser Ser His Gln Ser Ser Leu Ser Ala
            340                 345                 350

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Asn Thr Ala Asn Ser Leu Cys Leu Gly Gly Thr Pro Ala Ser Ala Ser
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Thr Gln Gly Thr Ala Ala Gly Asp Tyr Ser Lys Gly Gly Tyr Ala Gly
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Ser Ser Gln Ala Pro Asn Lys Ser Ala Gly Ser Gly Pro Gly Lys Gly
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Val Tyr Asn Lys Thr Gln Thr Phe Asp Lys Gln Gly Phe His Ala Gly
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<220>
<221> MISC_FEATURE
<223> a partial peptide of BPL1, which shows high homology with the pep
tide of SEQ ID NO:13

<400> 20

Ala Val Leu Cys Gln Val
1 5

<210> 21
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and KIAA1491(SEQ ID NO:6)

<400> 21

Gln Pro Ser Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro
1 5 10 15

Pro Ser Ser Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr
20 25 30

Leu

<210> 22
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA1491(SEQ ID NO:6) showing high score
in the local alignment between JNK3 and KIAA1491

<400> 22

Gln Ser Ser Ala Thr Phe Ser Thr Ala Ala Thr Ser Val Ser Ser Ser

1 5 10 15

Ala Ser Ser Gly Val Ser Leu Ser Ser Ser Met Asn Thr Ala Asn Ser
20 25 30

Leu

<210> 23
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and KIAA1491(SEQ ID NO:6)

<400> 23

Ser Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser
1 5 10 15

Ser Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu Ala
20 25 30

Ser Asp Thr Asp Ser Ser Leu Glu Ala Ser Ala
35 40

<210> 24
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA1491(SEQ ID NO:6) showing high score
in the local alignment between JNK3 and KIAA1491

<400> 24

Ala Ala Thr Ser Val Ser Ser Ser Ala Ser Ser Gly Val Ser Leu Ser
1 5 10 15

Ser Ser Met Asn Thr Ala Asn Ser Leu Cys Leu Gly Gly Thr Pro Ala
20 25 30

Ser Ala Ser Ser Ser Ser Ser Arg Ala Ala Pro
35 40

<210> 25
<211> 4
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial sequence identical in the sequences of JNK3 and KIAA1491(SEQ ID NO:6)

<400> 25

Phe Asp Lys Gln
1

<210> 26
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig nment between JNK3 and KIAA1491(SEQ ID NO:6)

<400> 26

His Ser Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn
1 5 10

<210> 27
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA1491(SEQ ID NO:6) showing high score in the local alignment between JNK3 and KIAA1491

<400> 27

His Pro Thr Thr Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr
1 5 10

<210> 28
<211> 4

<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial sequence identical in the sequences of JNK3 and KIAA1491(SEQ ID NO:6)

<400> 28

Asp Leu Lys Pro
1

<210> 29
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig nment between JNK3 and KIAA1491(SEQ ID NO:6)

<400> 29

Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser Ser
1 5 10 15

Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu
20 25 30

<210> 30
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA1491(SEQ ID NO:6) showing high score in the local alignment between JNK3 and KIAA1491

<400> 30

Pro Tyr Gln Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile
1 5 10 15

Met Asn Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu
20 25

<210> 31
<211> 4
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial sequence identical in the sequences of JNK3 and KIAA1491(SEQ ID NO:6)

<400> 31

Ser Ser Glu Ser
1

<210> 32
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig nment between JNK3 and KIAA1491(SEQ ID NO:6)

<400> 32

Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser Ser Ser
1 5 10 15

Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu Ala Ser Asp
20 25 30

Thr

<210> 33
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA1491(SEQ ID NO:6) showing high score in the local alignment between JNK3 and KIAA1491

<400> 33

Thr Gly Asp Leu Thr Ser Ser Pro Leu Ser Gln Leu Ser Ser Ser Leu
1 5 10 15

Ser Ser His Gln Ser Ser Leu Ser Ala His Ala Ala Leu Ser Ser Ser
20 25 30

Thr

<210> 34
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and KIAA1491(SEQ ID NO:6)

<400> 34

Pro Ser Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro
1 5 10 15

Ser Ser Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu
20 25 30

Ala Ser Asp Thr Asp Ser Ser Leu Glu Ala Ser Ala
35 40

<210> 35
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA1491(SEQ ID NO:6) showing high score
in the local alignment between JNK3 and KIAA1491

<400> 35

Ser Ser Pro Leu Ser Gln Leu Ser Ser Ser Leu Ser Ser His Gln Ser
1 5 10 15

Ser Leu Ser Ala His Ala Ala Leu Ser Ser Ser Thr Ser His Thr His
20 25 30

Ala Ser Val Glu Ser Ala Ser Ser His Gln Ser Ser Ala
35 40 45

<210> 36
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 36

Gln Pro Ser Pro Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro
1 5 10 15

Pro Ser Ser Ser Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln
20 25 30

<210> 37
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score
in the local alignment between JNK3 and KIAA0596

<400> 37

Gln Pro Pro Pro Pro Glu Lys Thr Pro Asn Pro Met Glu Cys Thr Lys
1 5 10 15

Pro Gly Ala Ala Leu Ser Gln Asp Ser Ala Val Ser Leu Glu Gln
20 25 30

<210> 38
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 38

Phe Thr Pro Gln Lys Thr Leu Glu Glu
1 5

<210> 39
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score in the local alignment between JNK3 and KIAA0596

<400> 39

Tyr Ser Leu Gln Gln Thr Leu Asp Glu
1 5

<210> 40
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 40

Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala
1 5 10 15

Gly Thr Ser Phe
20

<210> 41
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score in the local alignment between JNK3 and KIAA0596

<400> 41

Ser Asp Lys Asn Leu Ser Ile Phe Asp Phe Ser Ser Gly Glu Cys Val
1 5 10 15

Ala Thr Met Phe
20

<210> 42
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 42

Lys Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu
1 5 10 15

<210> 43
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score
in the local alignment between JNK3 and KIAA0596

<400> 43

Lys Leu Leu Ala Ser Ala Ser Arg Asp Arg Leu Ile His Val Leu
1 5 10 15

<210> 44
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 44

Ser Leu Phe Pro Ala Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln

1 5 10 15

Ala Arg Asp Leu Leu Ser Lys
20

<210> 45
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score in the local alignment between JNK3 and KIAA0596

<400> 45

Ser Leu Val Pro Gln Glu Arg His Glu Ala Ser Leu Gln Ala Pro Ser
1 5 10 15

Pro Gly Ala Leu Leu Ser Arg
20

<210> 46
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 46

Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu Val Met Asn Ser Glu
1 5 10 15

Glu

<210> 47
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score in the local alignment between JNK3 and KIAA0596

<400> 47

Leu Asp Lys Trp Val Glu Leu Arg Val Tyr Pro Glu Val Lys Asp Ser
1 5 10 15

Asn Gln

<210> 48
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and KIAA0596(SEQ ID NO:3)

<400> 48

Ser Ser Met Ser Thr Asp Gln Thr Leu Ala Ser Asp Thr Asp
1 5 10

<210> 49
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of KIAA0596(SEQ ID NO:3) showing high score in the local alignment between JNK3 and KIAA0596

<400> 49

Ser Met Leu Ser Pro Gly Pro Ala Leu Ser Ser Asp Ser Asp
1 5 10

<210> 50
<211> 23
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alignment between JNK3 and BMAL1

<400> 50

Ser Lys Ser Lys Val Asp Asn Gln Phe Tyr Ser Val Glu Val Gly Asp
1 5 10 15

Ser Thr Phe Thr Val Leu Lys
20

<210> 51
<211> 23
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL1 showing high score in the local ali
gnment between JNK3 and BMAL1

<400> 51

Thr Arg Glu Lys Ile Thr Thr Asn Cys Tyr Lys Phe Lys Ile Lys Asp
1 5 10 15

Gly Ser Phe Ile Thr Leu Arg
20

<210> 52
<211> 14
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BMAL1

<400> 52

Val Gly Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn
1 5 10

<210> 53
<211> 14
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature

<223> Partial oligopeptide of BMAL1 showing high score in the local ali
gnment between JNK3 and BMAL1

<400> 53

Val Ser Glu Ser Val Phe Lys Ile Leu Asn Tyr Ser Gln Asn
1 5 10

<210> 54
<211> 10
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BMAL1

<400> 54

Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe
1 5 10

<210> 55
<211> 10
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL1 showing high score in the local ali
gnment between JNK3 and BMAL1

<400> 55

Glu Leu Leu Gly Thr Ser Cys Tyr Glu Tyr
1 5 10

<210> 56
<211> 22
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BMAL1

<400> 56

Ser Ser Met Ser Thr Asp Gln Thr Leu Ala Ser Asp Thr Asp Ser Ser
1 5 10 15

Leu Glu Ala Ser Ala Gly
20

<210> 57
<211> 22
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL1 showing high score in the local ali
gnment between JNK3 and BMAL1

<400> 57

Ser Ser Pro Ser Asn Asp Glu Ala Ala Met Ala Val Ile Met Ser Leu
1 5 10 15

Leu Glu Ala Asp Ala Gly
20

<210> 58
<211> 10
<212> PRT

<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BMAL1

<400> 58

Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe
1 5 10

<210> 59
<211> 10
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL1 showing high score in the local ali
gnment between JNK3 and BMAL1

<400> 59

Ser Glu Ser Val Phe Lys Ile Leu Asn Tyr
1 5 10

<210> 60
<211> 10
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BMAL1

<400> 60

Tyr Ile Asp Gln Trp Asn Lys Val Ile Glu
1 5 10

<210> 61
<211> 10
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL1 showing high score in the local ali
gnment between JNK3 and BMAL1

<400> 61

Phe Met Asn Pro Trp Thr Lys Glu Val Glu
1 5 10

<210> 62
<211> 11
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BMAL1

<400> 62

Val Lys Gly Gln Pro Ser Pro Ser Gly Ala Ala
1 5 10

<210> 63
<211> 11
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL1 showing high score in the local ali
gnment between JNK3 and BMAL1

<400> 63

Val Lys Glu Gln Leu Ser Ser Ser Asp Thr Ala
1 5 10

<210> 64
<211> 31
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BMAL2

<400> 64

Glu Glu Lys Thr Lys Asn Gly Val Val Lys Gly Gln Pro Ser Pro Ser
1 5 10 15

Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser Ser Ser
20 25 30

<210> 65
<211> 31
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL2 showing high score in the local ali
gnment between JNK3 and BMAL2

<400> 65

Asp Asp Ser Ser Pro Thr Gly Leu Met Lys Asp Thr His Thr Val Asn
1 5 10 15

Cys Arg Ser Met Ser Asn Lys Glu Leu Phe Pro Pro Ser Pro Ser
20 25 30

<210> 66
<211> 10
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BMAL2

<400> 66

Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe
1 5 10

<210> 67
<211> 10
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL2 showing high score in the local ali
gnment between JNK3 and BMAL2

<400> 67

Glu Leu Leu Gly Thr Ser Cys Tyr Glu Tyr
1 5 10

<210> 68
<211> 23
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BMAL2

<400> 68

Ser Lys Ser Lys Val Asp Asn Gln Phe Tyr Ser Val Glu Val Gly Asp
1 5 10 15

Ser Thr Phe Thr Val Leu Lys
20

<210> 69
<211> 23
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL2 showing high score in the local ali
gnment between JNK3 and BMAL2

<400> 69

Ser Lys Glu Lys Ile Leu Thr Asp Ser Tyr Lys Phe Arg Ala Lys Asp
1 5 10 15

Gly Ser Phe Val Thr Leu Lys
20

<210> 70
<211> 12
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BMAL2

<400> 70

Ser Lys Ser Lys Val Asp Asn Gln Phe Tyr Ser Val
1 5 10

<210> 71
<211> 12
<212> PRT
<213> homo sapiens

<220>
<221> misc_feature
<223> Partial oligopeptide of BMAL2 showing high score in the local ali
gnment between JNK3 and BMAL2

<400> 71

Ser Lys Lys Lys Glu His Arg Lys Phe Tyr Thr Ile
1 5 10

<210> 72
<211> 8
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BPL1

<400> 72

Ser Tyr Leu Leu Tyr Gln Met Leu
1 5

<210> 73
<211> 8
<212> PRT
<213> homo sapiens

<220>

<221> MISC_FEATURE
<223> Partial oligopeptide of BPL1 showing high score in the local alig
nment between JNK3 and BPL1

<400> 73

Ser Tyr Ile Leu Tyr His Leu Leu
1 5

<210> 74
<211> 8
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BPL1

<400> 74

Ser Glu Pro Thr Leu Asp Val Lys
1 5

<210> 75
<211> 8
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of BPL1 showing high score in the local alig
nment between JNK3 and BPL1

<400> 75

Pro Glu Pro Ser Leu Glu Ile Lys
1 5

<210> 76
<211> 14
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BPL1

<400> 76

Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys Ser
1 5 10

<210> 77
<211> 14
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of BPL1 showing high score in the local alig
nment between JNK3 and BPL1

<400> 77

Val His Leu Glu Leu Pro Pro Ser Ser Asn Ile Val Gln Thr
1 5 10

<210> 78
<211> 9
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BPL1

<400> 78

Gln Lys Thr Leu Glu Glu Phe Gln Asp
1 5

<210> 79
<211> 9
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of BPL1 showing high score in the local alig
nment between JNK3 and BPL1

<400> 79

Glu Lys Leu Ile Lys Glu Phe Gln Asp
1 5

<210> 80
<211> 4
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial sequence identical in the sequences of JNK3 and BPL1

<400> 80

Glu Phe Gln Asp
1

<210> 81
<211> 12
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BPL1

<400> 81

Asp Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu
1 5 10

<210> 82
<211> 11
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of BPL1 showing high score in the local alig
nment between JNK3 and BPL1

<400> 82

Glu Ala Val Leu Cys Gln Val His Leu Glu Leu

1 5 10

<210> 83
<211> 4
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial sequence identical in the sequences of JNK3 and BPL1

<400> 83

Leu Cys Gln Val
1

<210> 84
<211> 7
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BPL1

<400> 84

Leu Pro Pro Ser Ser Ser Val
1 5

<210> 85
<211> 7
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of BPL1 showing high score in the local alig
nment between JNK3 and BPL1

<400> 85

Leu Pro Pro Ser Ser Asn Ile
1 5

<210> 86
<211> 5
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial sequence identical in the sequences of JNK3 and BPL1

<400> 86

Leu Pro Pro Ser Ser
1 5

<210> 87
<211> 15
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BPL1

<400> 87

Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu Val Met
1 5 10 15

<210> 88
<211> 15
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of BPL1 showing high score in the local alig
nment between JNK3 and BPL1

<400> 88

Ser Gln Glu Ala Leu Gly Arg Phe His Glu Val Arg Ser Val Leu
1 5 10 15

<210> 89
<211> 11
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of JNK3 showing high score in the local alig
nment between JNK3 and BPL1

<400> 89

Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu
1 5 10

<210> 90
<211> 11
<212> PRT
<213> homo sapiens

<220>
<221> MISC_FEATURE
<223> Partial oligopeptide of BPL1 showing high score in the local alig
nment between JNK3 and BPL1

<400> 90

Arg Ser Ile Pro Glu Tyr Gln Asp Ile Asn Leu
1 5 10

1